

## FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG  
CTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC  
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC  
AGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC  
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT  
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG  
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT  
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT  
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG  
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC  
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT  
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG  
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG  
AAACTAAGTAAATATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT  
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT  
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA  
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC  
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT  
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG  
AACCCTGAAGTTTTAAGTTTATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA  
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG  
TGTTGAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAACTCTGAATTC  
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG  
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCACTTCGGATGTGGGGTCAGGAGGTTG  
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA  
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACTATTAATAAATACCTT  
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT  
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP  
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL  
ATHFSNQNSGIIFFSSVETNIGNFFDVM TGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG  
NTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFS TFAGFLLFETK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Motif name: Clq domain signature.**

amino acids 137-167

**Clq domain proteins.**

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

10036344-19604

### FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG  
CTCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT  
GGGCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTT  
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC  
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA  
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACC  
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTG  
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA  
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTGAGCCACCTACTGCCTAGAATATAAAA  
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT  
GGCCGGGCGGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG  
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCTCTGAAGTACATGA  
CCAAGTGGATCCAGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC  
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA  
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC  
ACTCTGAGATATATAACAACTGAGCACAGTGAACACATGACTGTCTACGAGAAAGAAGCC  
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA  
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA  
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC  
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGT  
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT  
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC  
CACTGTGCCCTGGCACTGATTCTTCTCCTGCTTGCATAACTGATCATATTGCTTGTCTC  
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA  
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT  
TCTATACATAAAAGTTCCTACTTGTTAA

## **FIGURE 4**

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALESIPGFKEIVSRGVKVDY  
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLWWNGSEPLW  
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA  
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIIFSDHGMDIFW  
MDKVIELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY  
KKGK FVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP  
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVCMCLKGRAGTAPPVWPSHCALALI  
LLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

## FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC  
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG  
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA  
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG  
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG  
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC  
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT  
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG  
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT  
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT  
GCGTGCTGCCCCGTTCAGTTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC  
TCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACT  
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC  
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA  
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA  
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT  
TAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

## **FIGURE 6**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL  
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKL  
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVP  
VGCTCVLPRSV

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Tyrosine kinase phosphorylation site.**

amino acids 112-121

#### **N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

#### **Leucine zipper pattern.**

amino acids 3-25

#### **Homologous region to IL-17.**

amino acids 99-195

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## FIGURE 7

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAACATGCAGCTCGGCACTGGGCTCCTG  
CTGGCCGCCGTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCACCAGTGCAC  
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA  
CTGCCACCCGGGTCCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA  
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGAC  
CAGCCTCTGCAACCATGACTGACGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC  
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCCCTCCCTCGAGACTGGCCAGCCCACC  
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTAGGGAAGTCCTGCGTGAGTC  
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCCCTTCAGGTCCC  
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

403644-403644

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MLGTGLLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP

LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

1003644 1003644



## FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAG  
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCCCT  
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG  
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG  
CTGGGCTCGGGCGGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC  
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG  
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC  
TTCTGCCGCCGCGTGGTTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA  
CAAAATGGCCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT  
GTGAGAGTGAGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG  
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG  
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTG  
ATGGAAGCAATTCCCAGTACCGAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG  
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA  
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA  
ATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT  
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC  
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAAGTA  
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA  
GAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCTGGATC  
TGTATAAGGAATGGCATCAGAACAATAGCTTGGAATGGCTTGAAATCACAAAGGATCTGCAA  
GATGAACTGTAAGCTCCCCCTTGAGGCCAAATATTAAAGTAATTTTTATATGTCTATTATTC  
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC  
CCAACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC  
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTCATAAGTTGTTATCTA  
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA  
GTGTTTGATAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT  
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG  
TACCATAGAAAAAGTTTGTCTTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA  
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTC  
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA  
TTATTTTGTAGCTTAAATTAACAGATTTTGTAAATATGTAACCTTTGTTAATAGGTGCATAA  
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA  
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC  
TTGCCCCTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC  
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG  
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC  
ATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGATCG  
CATATTCATTGATGAGGGTTTGTCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC  
TAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAAGTCTCTGGTCTTCA  
TATGTCCTGTGCTCCTTTTAACCAAATAAAGAGTCTTGTCTTGGGGGAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADEFKHPCKMAYFHELSSRVSFQEARLACE  
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSAGCPDLYQWSDG  
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP  
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG  
RTKTSPNQSTLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

3063634.19901

# FIGURE 11

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
 CCACAGCCACTGGGCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTCTGTGCGAGGCCGGCAGGTGG  
 GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC  
 GGTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
 AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAACAGCAGATCTTCTCCGTTTCAGAGGACT  
 GCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
 GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG  
 TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
 TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
 CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC  
 ACAGAGCCATCACACAGAGTGGGGTCTCACCACCCAGGGATCATCGACTCTCACCCTTGGCCCCTAGCTCAGA  
 AAATCGCAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
 AAGACTGGTCTTAGCAAGAAGCTGAAAAATACATCTATCTCTCACCCTTGTATGGCACTGTCTTCCCCAAAA  
 GCCCCAAGGAACCTCTGAGGAGAAGCCCTTCCACTCTGTGCCCTTCCCTCATGGGTGTCAACAACCATGAGTTCA  
 GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
 CAACACCCGTCTTGACCACTGTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
 ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA  
 GTTTTTCAAGATACCTTCGAGATCTGGAAGCCCTGTCTTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
 CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTGCGAGGTCCCTTCCTCA  
 TGGACGAGAGCTCCCGCCTGGCCTTTCAGAGGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
 AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG  
 AACAAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTTCAGGGAGGCTGGATGCAGTTCTGGTCA  
 AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC  
 AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC  
 CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
 ATGTACAAGGCCGCTCCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT  
 CTTCTGTTAGTTCTAGACATCTCTAGCTTCTCTGAGGACTCACTCCCAGGAAGCCTTCCCTGCTTCTC  
 TGGGCTGTGCGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
 CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCAACCCACACAGGATCGGGTGGGA  
 CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAAGTGAAGTGAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
 CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
 AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC  
 TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA  
 ATCCATCAGGGCCATGAGTGTCAACCCAGACCTGACCCTCACCAATTCAGCCCCCTGACCCTCAGGACGCTGGATG  
 CCAGCTCCCAGCCCCAGTGCCGGGTCTCCCTCCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG  
 AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGGCTATTGTACA  
 GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGTTTTAGATGGAAGTGAGAG  
 GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTTCCCGCTCTGCCTGGGCTCCCACTTTGGCA  
 GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT  
 CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG  
 AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGGCCAGGCAGTGAGGGCCT  
 TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG  
 GACCTGCAGCCCTCCATGCCTGACCCTCCCCCAACCCCGTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAG  
 CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
 CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
 GGAATTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
 TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
 ACTCTGGTGGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
 TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAAACAGACCACTTGAATCTGTAAAT  
 GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
 CCCTCGGGTCCCCTCCCACGCCGTGGAAGCTTTGTTCTTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

300364-12601

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGVKGTDRLVNVFLG  
IPFAQPPPLGPDREFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC  
LVLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFF  
STGDEHAPGNQGF LDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPVAAGLF  
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT  
IYPLTVDGT VFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWLLDTMEQMSREDMLA  
ISTPVLTS LDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS  
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM  
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW  
HQQKQNRKAQEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 226-245

#### **N-glycosylation site.**

amino acids 105-109

#### **N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

#### **Carboxylesterases type-B serine active site.**

amino acids 216-232

Parameter	Unit	Value	Standard Error	t-value	p-value
$\alpha_1$		0.000	0.000	0.000	0.000
$\alpha_2$		0.000	0.000	0.000	0.000
$\alpha_3$		0.000	0.000	0.000	0.000
$\alpha_4$		0.000	0.000	0.000	0.000
$\alpha_5$		0.000	0.000	0.000	0.000
$\alpha_6$		0.000	0.000	0.000	0.000
$\alpha_7$		0.000	0.000	0.000	0.000
$\alpha_8$		0.000	0.000	0.000	0.000
$\alpha_9$		0.000	0.000	0.000	0.000
$\alpha_{10}$		0.000	0.000	0.000	0.000
$\alpha_{11}$		0.000	0.000	0.000	0.000
$\alpha_{12}$		0.000	0.000	0.000	0.000
$\alpha_{13}$		0.000	0.000	0.000	0.000
$\alpha_{14}$		0.000	0.000	0.000	0.000
$\alpha_{15}$		0.000	0.000	0.000	0.000
$\alpha_{16}$		0.000	0.000	0.000	0.000
$\alpha_{17}$		0.000	0.000	0.000	0.000
$\alpha_{18}$		0.000	0.000	0.000	0.000
$\alpha_{19}$		0.000	0.000	0.000	0.000
$\alpha_{20}$		0.000	0.000	0.000	0.000
$\alpha_{21}$		0.000	0.000	0.000	0.000
$\alpha_{22}$		0.000	0.000	0.000	0.000
$\alpha_{23}$		0.000	0.000	0.000	0.000
$\alpha_{24}$		0.000	0.000	0.000	0.000
$\alpha_{25}$		0.000	0.000	0.000	0.000
$\alpha_{26}$		0.000	0.000	0.000	0.000
$\alpha_{27}$		0.000	0.000	0.000	0.000
$\alpha_{28}$		0.000	0.000	0.000	0.000
$\alpha_{29}$		0.000	0.000	0.000	0.000
$\alpha_{30}$		0.000	0.000	0.000	0.000
$\alpha_{31}$		0.000	0.000	0.000	0.000
$\alpha_{32}$		0.000	0.000	0.000	0.000
$\alpha_{33}$		0.000	0.000	0.000	0.000
$\alpha_{34}$		0.000	0.000	0.000	0.000
$\alpha_{35}$		0.000	0.000	0.000	0.000
$\alpha_{36}$		0.000	0.000	0.000	0.000
$\alpha_{37}$		0.000	0.000	0.000	0.000
$\alpha_{38}$		0.000	0.000	0.000	0.000
$\alpha_{39}$		0.000	0.000	0.000	0.000
$\alpha_{40}$		0.000	0.000	0.000	0.000
$\alpha_{41}$		0.000	0.000	0.000	0.000
$\alpha_{42}$		0.000	0.000	0.000	0.000
$\alpha_{43}$		0.000	0.000	0.000	0.000
$\alpha_{44}$		0.000	0.000	0.000	0.000
$\alpha_{45}$		0.000	0.000	0.000	0.000
$\alpha_{46}$		0.000	0.000	0.000	0.000
$\alpha_{47}$		0.000	0.000	0.000	0.000
$\alpha_{48}$		0.000	0.000	0.000	0.000
$\alpha_{49}$		0.000	0.000	0.000	0.000
$\alpha_{50}$		0.000	0.000	0.000	0.000
$\alpha_{51}$		0.000	0.000	0.000	0.000
$\alpha_{52}$		0.000	0.000	0.000	0.000
$\alpha_{53}$		0.000	0.000	0.000	0.000
$\alpha_{54}$		0.000	0.000	0.000	0.000
$\alpha_{55}$		0.000	0.000	0.000	0.000
$\alpha_{56}$		0.000	0.000	0.000	0.000
$\alpha_{57}$		0.000	0.000	0.000	0.000
$\alpha_{58}$		0.000	0.000	0.0	

CATGGAGGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG  
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAA  
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCT  
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG  
ACAGAAATTACTTAGGGCTGAAGGAAGTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTG  
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC  
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT  
CTGAAGGAGAACCTGCATTTAGATTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAAT  
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC  
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG  
AGGATCTATTGAGAATGCCATTGCGTTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG  
GTCTCATTTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG  
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA  
ATGAAGGATTTTTTTTTTAATGTTATCTTGCTATTAAAGTGGTAATGAATGTTCCAGGATGAG  
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACT  
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG  
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT  
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG  
GAATAAAACACAAATGTTGAAAAATGTAAATATATATACATAGATTCAAATCCTTATATAT  
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCCTAGTGTTTT  
ACTATAACTGTCACTATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT  
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAAA

## FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL  
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES  
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP  
IEVIRPDIAALVRQVVIKKKEDL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

[illegible]

TGTCGCCTGGCCCTCGCCATGTCAGACACCCGCGAGCGCTCCCTTCCCCGCCGGCCCTCCTGCTTCTGCTGCTGCTGCTA  
CTGGGGGGGCGCCACGGCTCTTTTCTGAGGAGCCGCCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGATGAAG  
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCTTCAACCCGCTGTGCGCCAACCTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCGTACGACCCCAAGCACGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTTCACAGCT  
ACTGTTACCGACTTCTTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGT  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTT  
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAAC  
GACGTGGAGAGGCTCCCCCGCGTGCTGGAGAAGCAGTGGACGTCTCTCTGAAGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCATTTCTACTTCAACGTGCTGACGGTGTACGGCGCTGAGTTCAGCCTCGGGGGCCGCGCCGTG  
GTCCTGGCCGTTTTTTTCCACGCCACGAACAGCATCCCTGGCTCGGTGCTGTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG  
GTGCCTCGACCCCGGCCCGGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT  
GTCTTCTCGGGTCTGAGGCGGGGACGGTCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGGCCCGGCGGTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGGCTGCTGGCTGCCCTTCCCCCGCTGCGTGGTC  
CGAGTGCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCCGG  
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGCTGTG  
TCGGTGAACCTGCTGTGTAACGTGCTCGGTGGCGGCTTCTGTTGGTGGGAGCCGTGTTCCGGCTTCAGCGTGGG  
TGGGTTCGTGGGCTCGTGAGCGTGCAGCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT  
GGCGAGGCGGTGCTGAGCGTCAAGCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCCCGAGCAGACGCCGCTGCCGAGAAGCGC  
CTGCCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC  
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCGCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC  
CCCGACGGCCGCCTCTATGCTGCCCGGCCCGGCCGCGCCTCCACAGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGGCCCCCTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG  
CCCTGGAGCCCGCCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC  
CGCACCCACACGTTCAACAGCGGCGAGGCCCGGCCCTGGGACCGCCACCGCGGCTGCCACGCCCGCGGGCACA  
GACTTGGCCACCTCCTCCCCATATGGGGGGCGGACAGGACTCGCCCCCGCTGCCCTAGGCGGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACGAGCAGAGACGAGTGCAGAACCGCGGGGCCGGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTTCAGTTTTTGGTTTCTTTTTCGGTTTTTCTAAC  
AATTGCACAACCTCGTTTCTCGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGCTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCAGGCCCTGGCGTGTGTGGTGTGCG  
TGCGTGTGCGTGCCGTGTTTCGTGTGCAAGGGGCCGGGGAGGTGGGCGTGTGTGTGCGTGCAGCGAAGGCTGCTG  
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCAGAAGGCCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC  
CCCCCCCCACTCTGCAGAGGGAAGCGGGACAATGCCGGGGTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCCAGGTTGGTGGAGAGTCCATGCCACCCGCTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCAGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCCTCCCCAGCCCCCTCCCCATCAAT  
AAAACCTCTGTTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPPEPPPLSVAPRDYLNHYPVFVVGSGPGRLTPAEGA  
DDLNIQVRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG  
ECRNFKVLLLRDESTLFVCGSNAFNVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF  
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSFVYFFFREI  
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG  
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR  
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV  
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ  
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG  
TRAAFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW  
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGGPGGGGGGGGAGVPPEALLA  
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLPA  
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTG  
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG  
TDLAHLHPYGGADRTAPPVP

### Important features of the protein:

#### Signal peptide:

amino acids 1-25

#### Transmembrane domains:

amino acids 318-339, 598-617

#### N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

#### Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

#### N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885



## FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTCTCGGCCGGGACAGC  
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG  
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG  
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC  
ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT  
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG  
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT  
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT  
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGAC  
CGAAAAGATGGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT  
GGAAATTAAATTCAGGGCAACATGTGGCCAAATCCCATATATTTTAAAGGGCCGGTTT  
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC  
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA  
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA  
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT  
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT  
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT  
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG  
GAAACCATGGGCCGGGTAAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG  
GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC  
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC  
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTCATTTTTTGATTTCTT  
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC  
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG  
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT  
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAGCAGGACAAGAATTTG  
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACTTTTCCAGGAATAT  
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC  
TGAGGACGACCTCTTCCCTTGTAATTGCCATAGGAAAAAGACCAAAGATGAACTCTGATATG  
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT  
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA  
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA  
TAAAACCACCTTTATTTTAAAGGAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF  
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS  
PYILKGPVYHENCDCPLQDSAALREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR  
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS  
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR  
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV  
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKCLKWAKDHDEEAKK  
IAKAGQEFARNNLMGDDIFCYYFKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK  
KTKDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 302-306, 414-418

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

#### **Tyrosine kinase phosphorylation site.**

amino acids 341-348

#### **N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

#### **Endoplasmic reticulum targeting sequence.**

amino acids 499-504

## FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCCGCATCCA  
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTCGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAAT**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGGAACT  
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCCCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT  
CCCCTGTCTATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG  
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG  
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG  
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG  
TGTC CCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAGCT  
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCC  
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC  
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA  
CGTTTTCTGTTGGAATTCCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTG  
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG  
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC  
CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT  
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC  
CCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA  
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

[illegible]

```
><subunit 1 of 1, 310 aa, 1 stop
```

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP  
PLFSKVIVVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT  
GSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVS  
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPLIGQKLSEMDSVLMKIHT  
SLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Signal peptide:

Transmembrane domain:

N-glycosylation sites.

N-myristoylation sites.

Amidation site.

Cell attachment sequence.

amino acids 205-208

## FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC  
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT  
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL  
DTGYRAPVTLVVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA  
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR  
PSCTTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90

## FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG  
 GAAAGGACAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT  
 TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT  
 CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT  
 CCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT  
 GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAG  
 GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA  
 CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT  
 CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA  
 TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG  
 AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA  
 AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT  
 GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT  
 TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC  
 GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCCAGGCTCTGTATGAGACCCAGGC  
 TCCAGAAAACAGCCCCATTGGGTTTCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG  
 GAGTCAACGCGGAAGTATCCTATTCATTTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT  
 CAAATCAATCCTTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA  
 TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTCTGCAAGATGTAGGGTTT  
 TAGTGGAAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTTCCAAC  
 TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC  
 TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT  
 CTGTGGAGAATTTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG  
 TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACAT  
 AACGGTCCTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTCACCCAAACCTCCTACACCC  
 TGTTCTGTCGCGGAGAACAACAGCCCCGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGA  
 GACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCAAGACCCGCACCTGCC  
 CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCGCTGG  
 ACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGCTGGGCGCCACAGACCGCGGCTCCCCCGCG  
 CTGAGCAGAGAGGCGCTGGTGCAGCTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGT  
 GCTGTACCCGCTGCAGAACGGTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC  
 CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG  
 TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCGGTGTGTGGGCGCACAAATGGGGA  
 GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCGAGCCAAGCACAGGCTCGTGGTGGTGG  
 TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC  
 GGCTTCTCCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGCCAGGCCAGGCCGAGGC  
 CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCT  
 CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCG  
 TGCTCGGTGCCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCTT  
 GTCCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT  
 TCTTGAAACCAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT  
 TCCACCTTCCGAAATAGCTTTGGATTAAATATTCAGTAAAGTCTGTTTTTGTATTCATATAC  
 TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT  
 TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT  
 TTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTCTAAATGATAGTGT  
 AAGGTTTTAATCTTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT  
 CTGAGGTTTTGATTCAATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTG  
 TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT  
 CGTGTGTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC  
 TACTATGCTCATGACAAAATGAAACAAGCATATTGTGAGCAATACTGAACATCAATAATAC  
 CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT  
 CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA  
 ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAATAAAAAAAAAAAAAA

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2083	0.0
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2086	0.0
2087	0.0
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2089	0.0
2090	0.0
2091	0.0
2092	0.0
2093	0.0
2094	0.0
2095	0.0
2096	0.0
2097	0.0
2098	0.0
2099	0.0
2100	0.0

```
><subunit 1 of 1, 800 aa, 1 stop
```

MAVRELCFPRQRQVLF<sup>1</sup>FLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR  
GTRVVSDDNKQYLL<sup>2</sup>LLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRV  
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGG<sup>3</sup>LN<sup>4</sup>GIQNYTISPNSFFHINISGGD  
EGMIYPELVLDKALDREEQGELS<sup>5</sup>LT<sup>6</sup>LTALDGGSPSRSGTSTVRIVVL<sup>7</sup>LDVNDNAPQFAQALYE  
TQAPENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE  
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND  
RDSGENGMVCYIQENLPFL<sup>8</sup>LKPSVENFYILITEGALDREIRA<sup>9</sup>EYNITITVTDLGT<sup>10</sup>PRLKTE  
HNITVLVSDVNDNAPAF<sup>11</sup>TQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLASLV<sup>12</sup>SINADNGHLFALRSLDYEALQAFEF<sup>13</sup>RVGATDRGSPALSREALVRVLVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLV<sup>14</sup>DGFSQPYLPLPEAAPAQAAQ  
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFP<sup>15</sup>GH<sup>16</sup>LV<sup>17</sup>DVRGA  
ETLSOSYOYEVCLTGGPGTSEFKFLKPVISDIOAOGPGRKGEENSTFRNSFGFNIO

Signal peptide:

Transmembrane domain:

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

amino acids 28-32

**Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

## Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560



## FIGURE 25

GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC  
GTCTTCCTTCCGGGGGACAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCTCTTG  
GGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTC  
AGAACTCCAGCCTAATGGATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGGCTGTGCTG  
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCCGCCCCGGCGCTGTTAGAGAA  
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG  
CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATG  
GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTCC  
TCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTGGGGA  
GCGATCCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG  
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACG  
AGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG  
CCCTGGAGCAAGATCTTCCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAGGCTGGC  
TCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAAAGGACCGATTCTTCTCTGGTGTGGACTA  
CATTGTAATTTTCAAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC  
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC  
TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGA  
CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGG  
AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGT  
GAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT  
TTCTATTTCATGGGATCGAGGGCGCGTTTGATGAGCCTGGAATAAAACAGTCATACCTGGCC  
GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAA  
CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAACAAGATGGTTGT  
TTCCATGACTCTAGGACTACACCCGTGGATTGCAAATATTGATGACACCCAGTATCTCGCAG  
CAAAAAGAGCGATCAGAACAGTGTGGAACAGAACAGATATGATCCGGGATGGATCCACC  
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGG  
AGCTGTTGATGATGGAGAACATTTCGAGAATGAGAAAATCAACAGGTGGAATAACATAGAGG  
GAACCAAATTATTTGCTGCCTTTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCT  
TCTAGTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAAT  
GTAAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG  
GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCC  
CCCCTGCACACCTTCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCAAGTCCTGT  
GCAATAGCCCCAGGATTGGATTCCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGA  
TTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTGCTCGTGACACATAATCATTC  
ATCCAATGATCGCCTTTGCTTTACCACTCTTTCCTTTTATCTTATTAATAAAAAATGTTGGTC  
TCCACCACTGNCTCCCAA  
AAAAAAAAAA

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD  
SVQPVPFRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDQGQSLPIPPVILAEELGSDPTK  
GTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD  
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY  
FMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY  
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK  
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI  
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF  
A AFFLEMAQLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

273-292

#### **N-glycosylation sites.**

amino acids 322-326, 382-386, 402-406

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 400-404

#### **N-myristoylation sites.**

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,  
351-357

#### **Cell attachment sequence.**

amino acids 140-143

#### **ArgE / dapE / ACY1 / CPG:**

amino acids 156-167

100364-100364

## FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC  
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCTATGGGACCTGTGCGGTT  
GGGAATATTGCTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG  
AGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG  
CTACAGGCGGAAGTCTGAGTCGCACCGGTCTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT  
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG  
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA  
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG  
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT  
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC  
TTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC  
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA  
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG  
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTTTGACCCTTGCCTTTGAG  
CCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG  
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC  
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG  
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA  
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC  
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTTAGACCCTTCCAAGGAAGA  
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA  
GCAAACCGTGAAGGAGAATGGGACACTGGGTCTGGCCTGGAGTTGCTGATAATTTAGGTGG  
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT  
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL  
ELGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMTATLK  
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG  
HVLPAETAACLQETWTGKEITDGEEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

#### **N-myristoylation site.**

amino acids 115-121

#### **Amidation site.**

amino acids 70-74

FIGURE 28

## **FIGURE 29**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG  
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACCTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 169-173

#### **Tyrosine kinase phosphorylation site.**

amino acids 59-68

#### **N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

#### **Phosphatidylethanolamine signature.**

amino acids 113-157

## **FIGURE 31**

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA  
CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**ATG**AGAGGGCACTCCAGGAGACGCTGATGG  
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG  
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG  
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT  
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT  
CCACCCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC  
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA  
C**TGA**ACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT  
TTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG  
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG  
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCTCTCAAGCTGGTGCTGTGTAG  
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA  
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA  
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT  
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAACA  
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC  
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA  
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG  
ACCTTGTAACAATAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCCTAATTGTAATGTG  
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA  
ATAAAGAAAGAGTAAACTG

## **FIGURE 32**

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL  
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY  
NTAFELNIND

### **Signal sequence:**

amino acids 1-17

### **N-myristoylation site.**

amino acids 10-16

### **Cell attachment sequence.**

amino acids 36-39

403644-4304  
T0321-4304



Variable	Mean	SD	Min	Max
Age	33.1	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	10	25
Health status	1.2	0.8	0	3
Stress level	2.1	1.2	1	4
Life satisfaction	3.5	1.0	2	5
Work engagement	4.2	0.9	3	5
Organizational commitment	3.8	1.1	2	5
Job satisfaction	3.9	1.0	2	5
Turnover intention	1.5	0.7	0	3
Organizational citizenship behavior	2.8	0.9	1	4
Employee well-being	3.2	1.1	2	5
Work-life balance	3.1	1.0	2	4
Perceived organizational support	3.6	1.0	2	5
Psychological safety	3.4	1.0	2	5
Trust in supervisor	3.7	1.0	2	5
Trust in organization	3.5	1.0	2	5
Organizational justice	3.3	1.0	2	5
Employee voice	2.9	0.9	1	4
Employee silence	2.5	0.8	1	4
Employee engagement	4.1	0.9	3	5
Employee commitment	3.9	1.0	2	5
Employee satisfaction	3.8	1.0	2	5
Employee turnover	1.4	0.6	0	3
Employee retention	2.6	0.8	1	4
Employee loyalty	3.0	0.9	1	4
Employee citizenship	2.7	0.8	1	4
Employee well-being	3.2	1.1	2	5
Work-life balance	3.1	1.0	2	4
Perceived organizational support	3.6	1.0	2	5
Psychological safety	3.4	1.0	2	5
Trust in supervisor	3.7	1.0	2	5
Trust in organization	3.5	1.0	2	5
Organizational justice	3.3	1.0	2	5
Employee voice	2.9	0.9	1	4
Employee silence	2.5	0.8	1	4
Employee engagement	4.1	0.9	3	5
Employee commitment	3.9	1.0	2	5
Employee satisfaction	3.8	1.0	2	5
Employee turnover	1.4	0.6	0	3
Employee retention	2.6	0.8	1	4
Employee loyalty	3.0	0.9	1	4
Employee citizenship	2.7	0.8	1	4

Variable	Mean	SD	Min	Max
Age	33.1	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1.2	0.8	0.5	2.5
Health status	1.5	0.5	1	2
Stress level	2.5	1.0	1	4
Life satisfaction	3.5	1.0	1	5
Work satisfaction	3.0	1.0	1	5
Family satisfaction	3.5	1.0	1	5
Community satisfaction	3.0	1.0	1	5
Overall satisfaction	3.2	1.0	1	5

## FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY  
LDIHNYCVLDKLRDEFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEY  
IPVTTVLPDRQR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site.**

amino acids 60-69

**N-myristoylation site.**

amino acids 16-22

1003644.43001

## FIGURE 35

GTCTCCGCGTCACAGGAAGCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA  
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA  
GCCGCCCAGTCCCGGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTAC  
TCCTCCTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA  
AGCCGAGCGTGGAAGAATGCGGGTTCCTCGGGACCGGCACTTGGAATTCTGGTGTTAGTGCTCC  
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA  
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC  
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC  
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA  
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGTATCGATGA  
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC  
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT  
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT  
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT  
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG  
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG  
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA  
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG  
AAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC  
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT  
CCTACCTTGAAAAGCTTGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT  
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA  
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAA  
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT  
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA  
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA  
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA  
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAAACACTTC  
TAATTCTGTGATTAAAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT  
TAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT  
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 36**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN  
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK  
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA  
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDET  
VSNTLTLTNGLERRTKTYSIEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV  
KMMVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE  
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS  
KMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 37

GTGCTCCGGCGGCGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCTAGGCCCGGGCCACC**ATG**  
GCGCTGCCTCCAGGCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG  
CTCAGGTTGGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC  
GGGAGAATGAACGCCACGCCTTCACCTGCCGGGTGGCAGGGGGGCCTGGCACCCCCAGATTG  
GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG  
GGAGGCCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCCATCGGGCCCAGCATGAGC  
TCAACTGCTCTCTGCAGGACCCCAGAAGTGGCCGATCAGCCAACGCCTCTGTCTATCCTTAAT  
GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCAGG  
CCTCCTGGTTGTCTGTTTGCCCTGGTGCGTGCCAACCCGCCGGCCAATGTCACCTGGATCG  
ACCAGGATGGGCCAGTGACTGTCAACACCTCTGACTTCCTGGTGCTGGATGCGCAGAACTAC  
CCCTGGCTCACCAACCACACGGGTGCAGCTGCAGCTCCGCAGCCTGGCACACAACCTCTCGGT  
GGTGGCCACCAATGACGTGGGTGTCAACAGTGCGTTCCTTCCAGCCCCAGGCCCTCCCGGC  
ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAACTCAACAACGTGCGCCTGCCACGG  
GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGT  
GAAACCAGCAGACCGGCAGATGGCTCAGAACAACAGCCGGCCAGAGCTTCTGGACCCGGAGC  
CCGGCGGCCTCCTCACCAGCCAAGGTTTCATCCGCCTCCAGTGCTGGGCTATATCTATCGA  
GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTC**TGAG**CCGAGGGCGAGACAGGAGTATTCTC  
TTGGCCTCTGGACACCTCCCATTCCTCCAAGGCATCCTCTACCTAGCTAGGTCACCAACGT  
GAAGAAGTTATGCCACTGCCACTTTTGCTTGCCCTCCTGGCTGGGGTGCCCTCCATGTCTATG  
CACGTGATGCATTTCACTGGGCTGTAACCCGCAGGGGACAGGTATCTTTGGCAAGGCTACC  
AGTTGGACGTAAGCCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT  
CCAGAGGGAGCTCTTTGGCCAGGGGTGTTGAGATGTCATCCAGCATCCAAGTGTGGCATGGC  
CTGCTGTATACCCACCCCACTACTCCACAGCACCTTGTACAGTAGGCATGGGGGCGTGCCT  
GTGTGGGGGACAGGGAGGGGCCCTGCATGGATTTTCTCCTTCCTATGCTATGTAGCCTTGTT  
CCCTCAGGTAAAATTTAGGACCCTGCTAGCTGTGCAGAACCCAATTGCCCTTTGCACAGAAA  
CCAACCCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCCTTTTTTGCTGCACACGTCTCTG  
CCCTTCACTTCTTCTCTTCTGTCCCCACCTCCTCTTGGGAATTCTAGGTTACACGTTGGACC  
TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCAGTATTAG  
CACAAAGTTAGGGAGGAAGAGGCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGTAAGTA  
TGCATCATTTTCTACGGCGTTAGCACTTTAAGCACATCCCCTAGGGGAGGGGGTGAGTGAG  
GGGCCAGAGCCCTCTTTGTGGCTTCCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTC  
CTGAGCTCTCGGGGTTGATGGTTTTTCTCTCAGCATGTCTCCTCCACCACGGGACCCAGCC  
CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCTGGAGGATGGTCGCCACA  
GGCACATAATTCAACAGTGTGGAAGCTTTAGGGGAACATGGAGAAAGAAGGAGACCACATAC  
CCCAAAGTGACCTAAGAACAACCTTTAAAAAGCAACATGTAAATGATTGGAAATTAATATAGTA  
CAGAATATATTTTTCCCTTGTTGAGATCTTCTTTTGTAAATGTTTTTTCATGTTACTGCCTAGG  
GCGGTGCTGAGCACACAGCAAGTTTAATAAACTTGACTGAATTCATTTAAAAAAAAAAAAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 38**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR  
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL  
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN  
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLP  
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY  
RVSSVSSDEIWL

### **N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### **Glycosaminoglycan attachment site:**

amino acids 23-27

### **Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### **N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

## **FIGURE 39**

CGGGGACGGAAGCGGCCCCTGGGCCCAGGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGGC  
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

## **FIGURE 40**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFSPPL  
SNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 62-66

**N-myristoylation sites.**

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196

**Endoplasmic reticulum targeting sequence.**

amino acids 218-223



## **FIGURE 41**

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTGGAACCACAG  
ACGTGAGCCACTCCACCCAGCCTAAAACCTTCATCTTCTTTGGATGAGATGAACACTTTTAAC  
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT  
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA  
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT  
CGTCATCATGTCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA  
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG  
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTTCGTGCTTCTGAAAGGCTGGCTGAAAT  
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGGCCAAAAGTACTGCA  
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC  
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT  
TAGTGAGTCTCAGGTTTCCCAGACAACCTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA  
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG  
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC  
ACGAGCCAAGTACCTCAAGAGACATGGCTTCTAACATCTCAGATGAAACCCAAGACCATGAT  
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAACCTGGGAAT  
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAAAAAAAAAAAAAA

## **FIGURE 42**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE  
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-myristoylation sites.**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

#### **Amidation site.**

amino acids 40-44

FIGURE 42

## FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCCTCAGGACCCTCGCCATGAAAG  
CCCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC  
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG  
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT  
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG  
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC  
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAG  
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT  
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG  
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT  
CCCTTCCCACCTTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT  
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG  
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA  
AACCAGGCTCCCATATGTACCCCATCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA  
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN  
LRCGTPEEPCQEAFNQTNRKLGTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 77-81, 88-92

**N-myristoylation site.**

amino acids 84-90

**Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

FIGURE 44

## FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA  
GTCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT  
ACCGCACCCAGGTTCGGCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCCAT  
GGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC  
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA  
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA  
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCCAAAAGTCATACAGTGTC  
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA  
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT  
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC  
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCC  
TCGGCGGATTCCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT  
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC  
CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT  
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC  
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG  
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG  
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA  
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG  
GATATGGTGGTACCAGGAGACGATTAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT  
TTTGGAATTTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAG  
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTTGTATTCTATTATTTGAG  
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA  
TATTGCAGTTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAC  
CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA  
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA  
TTTGGTATTATATTATTTGATGTTTGTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA  
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG  
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA  
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC  
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## **FIGURE 46**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP  
QLKCVGGTAGCDSYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY  
VLRGSCGLEYNLDYTELGQLKESGKQHGFASFSDYYYKWSSADSCNMSGELITIVLLGIA  
FVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPYPPSYPGTWNRAYSPL  
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 171-190

### **N-glycosylation site.**

amino acids 172-176

### **Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

### **Tyrosine kinase phosphorylation site.**

amino acids 98-106

### **N-myristoylation sites.**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318